

SEQUENCE LISTING

<110> Behl, Christian
Klostermann, Andreas

<120> Human semaphorin 6A-1 (SEMA6A-A), a gene involved
in neuronal development and regeneration mechanisms
during apoptosis, and its use as a potential drug target

<130> 48498-258443

<140> 09/856,681

<141> 2001-05-22

<150> PCT/EP99/09215

<151> 1999-11-26

<150> 98122441.3

<151> 1998-11-26

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 3093

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(3093)

<400> 1

atg	agg	tca	gaa	gcc	ttg	ctg	cta	tat	ttc	aca	ctg	cta	cac	ttt	gct	48
Met	Arg	Ser	Glu	Ala	Leu	Leu	Leu	Tyr	Phe	Thr	Leu	Leu	His	Phe	Ala	
1				5					10					15		

ggg	gct	ggt	ttc	cca	gaa	gat	tct	gag	cca	atc	agt	att	tcg	cat	ggc	96
Gly	Ala	Gly	Phe	Pro	Glu	Asp	Ser	Glu	Pro	Ile	Ser	Ile	Ser	His	Gly	
			20					25					30			

aac	tat	aca	aaa	cag	tat	ccg	gtg	ttt	gtg	ggc	cac	aag	cca	gga	cgg	144
Asn	Tyr	Thr	Lys	Gln	Tyr	Pro	Val	Phe	Val	Gly	His	Lys	Pro	Gly	Arg	
			35				40					45				

aac	acc	aca	cag	agg	cac	agg	ctg	gac	atc	cag	atg	att	atg	atc	atg	192
Asn	Thr	Thr	Gln	Arg	His	Arg	Leu	Asp	Ile	Gln	Met	Ile	Met	Ile	Met	
		50				55					60					

aac	gga	acc	ctc	tac	att	gct	gct	agg	gac	cat	att	tat	act	gtt	gat	240
Asn	Gly	Thr	Leu	Tyr	Ile	Ala	Ala	Arg	Asp	His	Ile	Tyr	Thr	Val	Asp	
	65				70					75					80	

ata	gac	aca	tca	cac	acg	gaa	gaa	att	tat	tgt	agc	aaa	aaa	ctg	aca	288
Ile	Asp	Thr	Ser	His	Thr	Glu	Glu	Ile	Tyr	Cys	Ser	Lys	Lys	Leu	Thr	
				85					90					95		

tgg aaa tct aga cag gcc gat gta gac aca tgc aga atg aag gga aaa	336
Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys	
100 105 110	
cat aag gat gag tgc cac aac ttt att aaa gtt ctt cta aag aaa aac	384
His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn	
115 120 125	
gat gat gca ttg ttt gtc tgt gga act aat gcc ttc aac cct tcc tgc	432
Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys	
130 135 140	
aga aac tat aag atg gat aca ttg gaa cca ttc ggg gat gaa ttc agc	480
Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser	
145 150 155 160	
gga atg gcc aga tgc cca tat gat gcc aaa cat gcc aac gtt gca ctg	528
Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu	
165 170 175	
ttt gca gat gga aaa cta tac tca gcc aca gtg act gac ttc ctt gcc	576
Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala	
180 185 190	
att gac gca gtc att tac cgg agt ctt gga gaa agc cct acc ctg cgg	624
Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg	
195 200 205	
acc gtc aag cac gat tca aaa tgg ttg aaa gaa cca tac ttt gtt caa	672
Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln	
210 215 220	
gcc gtg gat tac gga gat tat atc tac ttc ttc ttc agg gaa ata gca	720
Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala	
225 230 235 240	
gtg gag tat aac acc atg gga aag gta gtt ttc cca aga gtg gct cag	768
Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln	
245 250 255	
gtt tgt aag aat gat atg gga gga tct caa aga gtc ctg gag aaa cag	816
Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln	
260 265 270	
tgg acg tgc ttc ctg aag gcg cgc ttg aac tgc tca gtt cct gga gac	864
Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp	
275 280 285	
tct cat ttt tat ttc aac att ctc cag gca gtt aca gat gtg att cgt	912
Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg	
290 295 300	
atc aac ggg cgt gat gtt gtc ctg gca acg ttt tct aca cct tat aac	960
Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn	
305 310 315 320	
agc atc cct ggg tct gca gtc tgt gcc tat gac atg ctt gac att gcc	1008
Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala	
325 330 335	

agt gtt ttt act ggg aga ttc aag gaa cag aag tct cct gat tcc acc	1056
Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr	
340 345 350	
tggtg aca cca gtt cct gat gaa cga gtt cct aag ccc agg cca ggt tgc	1104
Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys	
355 360 365	
tgt gct ggc tca tcc tcc tta gaa aga tat gca acc tcc aat gag ttc	1152
Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe	
370 375 380	
cct gat gat acc ctg aac ttc atc aag acg cac ccg ctc atg gat gag	1200
Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu	
385 390 395 400	
gca gtg ccc tcc atc ttc aac agg cca tgg ttc ctg aga aca atg gtc	1248
Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val	
405 410 415	
aga tac cgc ctt acc aaa att gca gtg gac aca gct gct ggg cca tat	1296
Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr	
420 425 430	
cag aat cac act gtg gtt ttt ctg gga tca gag aag gga atc atc ttg	1344
Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu	
435 440 445	
aag ttt ttg gcc aga ata gga aat agt ggt ttt cta aat gac agc ctt	1392
Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu	
450 455 460	
ttc ctg gag gag atg agt gtt tac aac tct gaa aaa tgc agc tat gat	1440
Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp	
465 470 475 480	
gga gtc gaa gac aaa agg atc atg ggc atg cag ctg gac aga gca agc	1488
Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser	
485 490 495	
agc tct ctg tat gtt gcg ttc tct acc tgt gtg ata aag gtt ccc ctt	1536
Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu	
500 505 510	
ggc cgg tgt gaa cga cat ggg aag tgt aaa aaa acc tgt att gcc tcc	1584
Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser	
515 520 525	
aga gac cca tat tgt gga tgg ata aag gaa ggt ggt gcc tgc agc cat	1632
Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His	
530 535 540	
tta tca ccc aac agc aga ctg act ttt gag cag gac ata gag cgt ggc	1680
Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly	
545 550 555 560	

aat aca gat ggt ctg ggg gac tgt cac aat tcc ttt gtg gca ctg aat Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn 565 570 575	1728
ggg cat tcc agt tcc ctc ttg ccc agc aca acc aca tca gat tcg acg Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr 580 585 590	1776
gct caa gag ggg tat gag tct agg gga gga atg ctg gac tgg aag cat Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His 595 600 605	1824
ctg ctt gac tca cct gac agc aca gac cct ttg ggg gca gtg tct tcc Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser 610 615 620	1872
cat aat cac caa gac aag aag gga gtg att cgg gaa agt tac ctc aaa His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys 625 630 635 640	1920
ggc cac gac cag ctg gtt ccc gtc acc ctc ttg gcc att gca gtc atc Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile 645 650 655	1968
ctg gct ttc gtc atg ggg gcc gtc ttc tcg ggc atc acc gtc tac tgc Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys 660 665 670	2016
gtc tgt gat cat cgg cgc aaa gac gtg gct gtg gtg cag cgc aag gag Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu 675 680 685	2064
aag gag ctc acc cac tcg cgc cgg ggc tcc atg agc agc gtc acc aag Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys 690 695 700	2112
ctc agc ggc ctc ttt ggg gac act caa tcc aaa gac cca aag ccg gag Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu 705 710 715 720	2160
gcc atc ctc acg cca ctc atg cac aac ggc aag ctc gcc act ccc ggc Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly 725 730 735	2208
aac acg gcc aag atg ctc att aaa gca gac cag cac cac ctg gac ctg Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu 740 745 750	2256
acg gcc ctc ccc acc cca gag tca acc cca acg ctg cag cag aag cgg Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg 755 760 765	2304
aag ccc agc cgc ggc agc cgc gag tgg gag agg aac cag aac ctc atc Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile 770 775 780	2352
aat gcc tgc aca aag gac atg ccc ccc atg ggc tcc cct gtg att ccc Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro 785 790 795 800	2400

acg gac ctg ccc ctg cgg gcc tcc ccc agc cac atc ccc agc gtg gtg	2448
Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val	
805 810 815	
gtc ctg ccc atc acg cag cag ggc tac cag cat gag tac gtg gac cag	2496
Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln	
820 825 830	
ccc aaa atg agc gag gtg gcc cag atg gcg ctg gag gac cag gcc gcc	2544
Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala	
835 840 845	
aca ctg gag tat aag acc atc aag gaa cat ctc agc agc aag agt ccc	2592
Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro	
850 855 860	
aac cat ggg gtg aac ctt gtg gag aac ctg gac agc ctg ccc ccc aaa	2640
Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys	
865 870 875 880	
gtt cca cag cgg gag gcc tcc ctg ggt ccc ccg gga gcc tcc ctg tct	2688
Val Pro Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser Leu Ser	
885 890 895	
cag acc ggt cta agc aag cgg ctg gaa atg cac cac tcc tct tcc tac	2736
Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Ser Tyr	
900 905 910	
ggg gtt gac tat aag agg agc tac ccc acg aac tcg ctc acg aga agc	2784
Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr Arg Ser	
915 920 925	
cac cag gcc acc act ctc aaa aga aac aac act aac tcc tcc aat tcc	2832
His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser	
930 935 940	
tct cac ctc tcc aga aac cag agc ttt ggc agg gga gac aac ccg ccg	2880
Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro	
945 950 955 960	
ccc gcc ccg cag agg gtg gac tcc atc cag gtg cac agc tcc cag cca	2928
Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro	
965 970 975	
tct ggc cag gcc gtg act gtc tcg agg cag ccc agc ctc aac gcc tac	2976
Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr	
980 985 990	
aac tca ctg aca agg tcg ggg ctg aag cgt acg ccc tcg cta aag ccg	3024
Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro	
995 1000 1005	
gac gta ccc ccc aaa cca tcc ttt gct ccc ctt tcc aca tcc atg aag	3072
Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met Lys	
1010 1015 1020	

ccc aat gat gcg tgt aca taa
 Pro Asn Asp Ala Cys Thr
 1025 1030

<210> 2
 <211> 1030
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala
 1 5 10 15
 Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
 20 25 30
 Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
 35 40 45
 Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
 50 55 60
 Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
 65 70 75 80
 Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
 85 90 95
 Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
 100 105 110
 His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
 115 120 125
 Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
 130 135 140
 Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
 145 150 155 160
 Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
 165 170 175
 Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
 180 185 190
 Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
 195 200 205
 Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
 210 215 220
 Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala
 225 230 235 240
 Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
 245 250 255

Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
 260 265 270
 Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
 275 280 285
 Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
 290 295 300
 Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
 305 310 315 320
 Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
 325 330 335
 Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
 340 345 350
 Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
 355 360 365
 Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
 370 375 380
 Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
 385 390 395 400
 Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
 405 410 415
 Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
 420 425 430
 Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
 435 440 445
 Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
 450 455 460
 Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
 465 470 475 480
 Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser
 485 490 495
 Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
 500 505 510
 Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
 515 520 525
 Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
 530 535 540
 Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
 545 550 555 560
 Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
 565 570 575

Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr
 580 585 590
 Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
 595 600 605
 Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
 610 615 620
 His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
 625 630 635 640
 Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile
 645 650 655
 Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys
 660 665 670
 Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu
 675 680 685
 Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys
 690 695 700
 Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu
 705 710 715 720
 Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly
 725 730 735
 Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu
 740 745 750
 Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg
 755 760 765
 Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile
 770 775 780
 Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro
 785 790 795 800
 Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val
 805 810 815
 Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln
 820 825 830
 Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala
 835 840 845
 Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro
 850 855 860
 Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys
 865 870 875 880

Val Pro Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser Leu Ser
885 890 895

Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Ser Tyr
900 905 910

Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr Arg Ser
915 920 925

His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser
930 935 940

Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro
945 950 955 960

Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro
965 970 975

Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr
980 985 990

Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro
995 1000 1005

Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met Lys
1010 1015 1020

Pro Asn Asp Ala Cys Thr
025 1030

<210> 3
<211> 216
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(216)

<400> 3
ccg ccg ccc gcc ccg cag agg gtg gac tcc atc cag gtg cac agc tcc 48
Pro Pro Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser
1 5 10 15

cag cca tct ggc cag gcc gtg act gtc tcg agg cag ccc agc ctc aac 96
Gln Pro Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn
20 25 30

gcc tac aac tca ctg aca agg tcg ggg ctg aag cgt acg ccc tcg cta 144
Ala Tyr Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu
35 40 45

aag ccg gac gta ccc ccc aaa cca tcc ttt gct ccc ctt tcc aca tcc 192
Lys Pro Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser
50 55 60

atg aag ccc aat gat gcg tgt aca
 Met Lys Pro Asn Asp Ala Cys Thr
 65 70

<210> 4
 <211> 72
 <212> PRT
 <213> Homo sapiens

<400> 4
 Pro Pro Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser
 1 5 10 15
 Gln Pro Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn
 20 25 30
 Ala Tyr Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu
 35 40 45
 Lys Pro Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser
 50 55 60
 Met Lys Pro Asn Asp Ala Cys Thr
 65 70

<210> 5
 <211> 65
 <212> PRT
 <213> Homo sapiens

<400> 5
 Pro Pro Pro Gln Pro Gln Arg Lys Pro Gln Val Gln Leu His Val Gln
 1 5 10 15
 Pro Gln Ala Lys Pro His Val Gln Pro Gln Pro Val Ser Ser Ala Asn
 20 25 30
 Thr Gln Pro Arg Gly Pro Leu Ser Gln Ala Pro Thr Pro Ala Pro Lys
 35 40 45
 Phe Ala Pro Val Ala Pro Lys Phe Thr Pro Val Val Ser Lys Phe Ser
 50 55 60
 Pro
 65

<210> 6
 <211> 3862
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (658)..(3750)

<400> 6
ggcacgaggc tgcagccaac tccgctcccc gcgcactcgg ctgcccagge gctcggaacc 60
cagcagcggc gctcctccgc ggtgccggtc gcccgcgatg cccgcttagc agcgtgtagc 120
agcggccagc atcaccacac ccgcggcacc gcgctgccgg ccgcagagcc gggccagagc 180
cttgcccccc tccccagcc cccacccgc cccccgcctt gaaatgactt gttaatcggc 240
gcagacacca ccaaggggac tcaccgaagt ggaatccaag tggaatttgg atttgagaa 300
gagtttcttg aacatttacc ctcttccttg ttggttttct ttttcttttt cttctttttt 360
tttttggtt ctttttctt ctccccctt ccgctcgtca ttggagatga acacatcgcg 420
tttgcattcc agaaagtagt cgccgcgact atttccccca aagagacaag cacacatgta 480
ggaatgacaa aggcttgcca aggagagagc cgcagccgcg gcccgagag atcccctcga 540
taatggatta ctaaattggga tacacgctgt accagttcgc tccgagcccc ggccgcctgt 600
ccgtcgatgc accgaaaagg gtgaagtaga gaaataaagt ctccccgctg aactact 657
atg agg tca gaa gcc ttg ctg cta tat ttc aca ctg cta cac ttt gct 705
Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala
1 5 10 15
ggg gct ggt ttc cca gaa gat tct gag cca atc agt att tcg cat ggc 753
Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
20 25 30
aac tat aca aaa cag tat ccg gtg ttt gtg ggc cac aag cca gga cgg 801
Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
35 40 45
aac acc aca cag agg cac agg ctg gac atc cag atg att atg atc atg 849
Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
50 55 60
aac gga acc ctc tac att gct gct agg gac cat att tat act gtt gat 897
Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
65 70 75 80
ata gac aca tca cac acg gaa gaa att tat tgt agc aaa aaa ctg aca 945
Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
85 90 95
tgg aaa tct aga cag gcc gat gta gac aca tgc aga atg aag gga aaa 993
Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
100 105 110
cat aag gat gag tgc cac aac ttt att aaa gtt ctt cta aag aaa aac 1041
His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
115 120 125
gat gat gca ttg ttt gtc tgt gga act aat gcc ttc aac cct tcc tgc 1089
Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
130 135 140

aga aac tat aag atg gat aca ttg gaa cca ttc ggg gat gaa ttc agc	1137
Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser	
145 150 155 160	
gga atg gcc aga tgc cca tat gat gcc aaa cat gcc aac gtt gca ctg	1185
Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu	
165 170 175	
ttt gca gat gga aaa cta tac tca gcc aca gtg act gac ttc ctt gcc	1233
Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala	
180 185 190	
att gac gca gtc att tac cgg agt ctt gga gaa agc cct acc ctg cgg	1281
Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg	
195 200 205	
acc gtc aag cac gat tca aaa tgg ttg aaa gaa cca tac ttt gtt caa	1329
Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln	
210 215 220	
gcc gtg gat tac gga gat tat atc tac ttc ttc ttc agg gaa ata gca	1377
Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala	
225 230 235 240	
gtg gag tat aac acc atg gga aag gta gtt ttc cca aga gtg gct cag	1425
Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln	
245 250 255	
gtt tgt aag aat gat atg gga gga tct caa aga gtc ctg gag aaa cag	1473
Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln	
260 265 270	
tgg acg tcg ttc ctg aag gcg cgc ttg aac tgc tca gtt cct gga gac	1521
Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp	
275 280 285	
tct cat ttt tat ttc aac att ctc cag gca gtt aca gat gtg att cgt	1569
Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg	
290 295 300	
atc aac ggg cgt gat gtt gtc ctg gca acg ttt tct aca cct tat aac	1617
Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn	
305 310 315 320	
agc atc cct ggg tct gca gtc tgt gcc tat gac atg ctt gac att gcc	1665
Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala	
325 330 335	
agt gtt ttt act ggg aga ttc aag gaa cag aag tct cct gat tcc acc	1713
Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr	
340 345 350	
tgg aca cca gtt cct gat gaa cga gtt cct aag ccc agg cca ggt tgc	1761
Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys	
355 360 365	

tgt gct ggc tca tcc tcc tta gaa aga tat gca acc tcc aat gag ttc	1809
Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe	
370 375 380	
cct gat gat acc ctg aac ttc atc aag acg cac ccg ctc atg gat gag	1857
Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu	
385 390 395 400	
gca gtg ccc tcc atc ttc aac agg cca tgg ttc ctg aga aca atg gtc	1905
Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val	
405 410 415	
aga tac cgc ctt acc aaa att gca gtg gac aca gct gct ggg cca tat	1953
Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr	
420 425 430	
cag aat cac act gtg gtt ttt ctg gga tca gag aag gga atc atc ttg	2001
Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu	
435 440 445	
aag ttt ttg gcc aga ata gga aat agt ggt ttt cta aat gac agc ctt	2049
Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu	
450 455 460	
ttc ctg gag gag atg agt gtt tac aac tct gaa aaa tgc agc tat gat	2097
Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp	
465 470 475 480	
gga gtc gaa gac aaa agg atc atg ggc atg cag ctg gac aga gca agc	2145
Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser	
485 490 495	
agc tct ctg tat gtt gcg ttc tct acc tgt gtg ata aag gtt ccc ctt	2193
Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu	
500 505 510	
ggc cgg tgt gaa cga cat ggg aag tgt aaa aaa acc tgt att gcc tcc	2241
Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser	
515 520 525	
aga gac cca tat tgt gga tgg ata aag gaa ggt ggt gcc tgc agc cat	2289
Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His	
530 535 540	
tta tca ccc aac agc aga ctg act ttt gag cag gac ata gag cgt ggc	2337
Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly	
545 550 555 560	
aat aca gat ggt ctg ggg gac tgt cac aat tcc ttt gtg gca ctg aat	2385
Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn	
565 570 575	
ggg cat tcc agt tcc ctc ttg ccc agc aca acc aca tca gat tgc acg	2433
Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr	
580 585 590	
gct caa gag ggg tat gag tct agg gga gga atg ctg gac tgg aag cat	2481
Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His	
595 600 605	

ctg ctt gac tca cct gac agc aca gac cct ttg ggg gca gtg tct tcc Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser 610 615 620	2529
cat aat cac caa gac aag aag gga gtg att cgg gaa agt tac ctc aaa His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys 625 630 635 640	2577
ggc cac gac cag ctg gtt ccc gtc acc ctc ttg gcc att gca gtc atc Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile 645 650 655	2625
ctg gct ttc gtc atg ggg gcc gtc ttc tcg ggc atc acc gtc tac tgc Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys 660 665 670	2673
gtc tgt gat cat cgg cgc aaa gac gtg gct gtg gtg cag cgc aag gag Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu 675 680 685	2721
aag gag ctc acc cac tcg cgc cgg gcc tcc atg agc agc gtc acc aag Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys 690 695 700	2769
ctc agc ggc ctc ttt ggg gac act caa tcc aaa gac cca aag ccg gag Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu 705 710 715 720	2817
gcc atc ctc acg cca ctc atg cac aac ggc aag ctc gcc act ccc ggc Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly 725 730 735	2865
aac acg gcc aag atg ctc att aaa gca gac cag cac cac ctg gac ctg Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu 740 745 750	2913
acg gcc ctc ccc acc cca gag tca acc cca acg ctg cag cag aag cgg Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg 755 760 765	2961
aag ccc agc cgc ggc agc cgc gag tgg gag agg aac cag aac ctc atc Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile 770 775 780	3009
aat gcc tgc aca aag gac atg ccc ccc atg ggc tcc cct gtg att ccc Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro 785 790 795 800	3057
acg gac ctg ccc ctg cgg gcc tcc ccc agc cac atc ccc agc gtg gtg Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val 805 810 815	3105
gtc ctg ccc atc acg cag cag ggc tac cag cat gag tac gtg gac cag Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln 820 825 830	3153

ccc aaa atg agc gag gtg gcc cag atg gcg ctg gag gac cag gcc gcc 3201
 Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala
 835 840 845

aca ctg gag tat aag acc atc aag gaa cat ctc agc agc aag agt ccc 3249
 Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro
 850 855 860

aac cat ggg gtg aac ctt gtg gag aac ctg gac agc ctg ccc ccc aaa 3297
 Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys
 865 870 875 880

gtt cca cag cgg gag gcc tcc ctg ggt ccc ccg gga gcc tcc ctg tct 3345
 Val Pro Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser Leu Ser
 885 890 895

cag acc ggt cta agc aag cgg ctg gaa atg cac cac tcc tct tcc tac 3393
 Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Ser Tyr
 900 905 910

ggg gtt gac tat aag agg agc tac ccc acg aac tcg ctc acg aga agc 3441
 Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr Arg Ser
 915 920 925

cac cag gcc acc act ctc aaa aga aac aac act aac tcc tcc aat tcc 3489
 His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser
 930 935 940

tct cac ctc tcc aga aac cag agc ttt ggc agg gga gac aac ccg ccg 3537
 Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro
 945 950 955 960

ccc gcc ccg cag agg gtg gac tcc atc cag gtg cac agc tcc cag cca 3585
 Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro
 965 970 975

tct ggc cag gcc gtg act gtc tcg agg cag ccc agc ctc aac gcc tac 3633
 Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr
 980 985 990

aac tca ctg aca agg tcg ggg ctg aag cgt acg ccc tcg cta aag ccg 3681
 Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro
 995 1000 1005

gac gta ccc ccc aaa cca tcc ttt gct ccc ctt tcc aca tcc atg aag 3729
 Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met Lys
 1010 1015 1020

ccc aat gat gcg tgt aca taa tcccaggggg aggggggtcag gtgtcgaacc 3780
 Pro Asn Asp Ala Cys Thr
 1025 1030

agcaggcaag gcgagggtgcc cgctcagctc agcaagggttc tcaactgcct cgagtaccca 3840

ccagaccaag aaggcctgcg gc 3862

<212> PRT

<213> Homo sapiens

<400> 7

```

Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala
 1           5           10           15

Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
          20           25           30

Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
          35           40           45

Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
          50           55           60

Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
          65           70           75           80

Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
          85           90           95

Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
          100          105          110

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
          115          120          125

Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
          130          135          140

Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
          145          150          155          160

Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
          165          170          175

Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
          180          185          190

Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
          195          200          205

Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
          210          215          220

Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala
          225          230          235          240

Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
          245          250          255

Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
          260          265          270

Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
          275          280          285

```


Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
 290 295 300
 Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
 305 310 315 320
 Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
 325 330 335
 Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
 340 345 350
 Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
 355 360 365
 Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
 370 375 380
 Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
 385 390 395 400
 Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
 405 410 415
 Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
 420 425 430
 Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
 435 440 445
 Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
 450 455 460
 Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
 465 470 475 480
 Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser
 485 490 495
 Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
 500 505 510
 Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
 515 520 525
 Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
 530 535 540
 Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
 545 550 555 560
 Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
 565 570 575
 Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr
 580 585 590
 Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
 595 600 605

Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
 610 615 620
 His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
 625 630 635 640
 Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile
 645 650 655
 Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys
 660 665 670
 Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu
 675 680 685
 Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys
 690 695 700
 Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu
 705 710 715 720
 Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly
 725 730 735
 Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu
 740 745 750
 Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg
 755 760 765
 Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile
 770 775 780
 Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro
 785 790 795 800
 Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val
 805 810 815
 Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln
 820 825 830
 Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala
 835 840 845
 Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro
 850 855 860
 Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys
 865 870 875 880
 Val Pro Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser Leu Ser
 885 890 895
 Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Ser Tyr
 900 905 910

Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr Arg Ser
 915 920 925

His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser
 930 935 940

Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro
 945 950 955 960

Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro
 965 970 975

Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr
 980 985 990

Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro
 995 1000 1005

Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met Lys
 1010 1015 1020

Pro Asn Asp Ala Cys Thr
 025 1030